AMENDMENTS TO THE SPECIFICATION

Please delete the paper copy of the Sequence Listing previously submitted in the present application and replace with the Sequence Listing submitted herewith in electronic format *via* EFS-Web.

In the specification at page 1, after the section entitled "RELATED APPLICATIONS" added in the Preliminary Amendment dated September 1, 2006, please insert the following new paragraph:

SEQUENCE LISTING SUBMISSION

The Sequence Listing associated with this application is filed in electronic format *via* EFS-Web and hereby incorporated by reference into the specification in its entirety. The name of the text file containing the Sequence Listing is Sequence_Listing_13987_00021. The size of the text file is 49 KB, and the text file was created on June 30, 2008.

In the specification at page 7, line 26, please replace the paragraph which starts with "Fig. 6a+b" with the following amended paragraph:

Fig. 6a+b: Protein alignment of the ptxA protein with the MSPRP2 protein from *Medicago sativa* and other similar proteins.

A: ptxA protein, GenBank Acc.-No.: X67427 (SEQ ID NO: 20)

B: *Medicago sativa* proline-rich cell wall protein GenBank Acc.-No.: AF028841 (SEQ ID NO: 21)

C: SEQ ID NO: 22

~~C~~ D: *Lycopersicum esculentum* proline rich protein GenBank Acc.-No.: X57076 (SEQ ID NO: 23)

~~D~~ E: *Vitis vinifera* proline-rich protein 1 (PRP1) GenBank Acc.-No.: AY046416 (SEQ ID NO: 24)

~~E~~ F: *Arabidopsis thaliana* protease inhibitor/seed storage/lipid transfer protein (LTP) GenBank Acc.-No.: NM104929 (SEQ ID NO: 25)

Consensus: SEQ ID NO: 26

In the specification at page 7, line 37, please replace the paragraph which starts with "Fig. 7a+b" with the following amended paragraph:

Fig. 7a+b: Alignment of the promoter regions of ptxA gene (A, SEQ ID NO: 87) and the MSPRP2 gene from *Medicago sativa* (B, SEQ ID NO: 27), consensus: SEQ ID NO: 28.

In the specification at page 7, line 40, please replace the paragraph which starts with "Fig. 8a-c" with the following amended paragraph:

Fig. 8a-c: Alignment of the SbHRGP3 promoter variations (consensus: SEQ ID NO: 29).

In the specification at page 51, line 18, please replace the paragraph which starts with "Genomic DNA" with the following amended paragraph:

Genomic DNA from pea and soybean is extracted using the ~~Qiagen~~ QIAGEN nucleic acid purification column (~~DNAeasy~~ DNeasy® Plant Mini Kit, (Qiagen). The ptxA promoter region region including the 5'-untranslated region (882 bp) and the SbHRGP3 promoter region including the 5'-untranslated region (1380 bp), respectively, wereas isolated from genomic DNA of pea (*Pisum sativum*) or soybean (*Glycine max*), respectively, using conventional PCR. Approximately 0.1 µg of digested genomic DNA was useds for the regular PCR reaction (see below). The primers were designed based on the pea ptxA sequence disclosed by Bown (GeneBank accession number X67427.1) and the SbHRGP3 sequence disclosed by Ahn (GenBank Acc.-No.: U44838), respectively. One µL of the diluted digested genomic DNA was used as the DNA template in the primary PCR reaction. The reaction comprised primers primer 1 (SEQ ID NO:13) and primer 2 (SEQ ID NO:24 or 11) for amplification of the ptxA promoter, or primers primer 1 (SEQ ID NO: 5) and primer 2 (SEQ ID NO: 6 or 11) for amplification of the SbHRGP3 promoter, respectively, in a mixture containing Buffer 3 following the protocol outlined by an Expand Long PCR kit (Cat #1681-842, Roche-Boehringer Mannheim). The isolated DNA is employed as template DNA in a PCR amplification reaction using the following primers:

In the specification at page 52, line 23, please replace the paragraph which starts with "The PCR product" with the following amended paragraph:

The PCR product is applied to a 1% (w/v) agarose gel and separated at 80V. Fragments of approximately 882 base pairs in length are excised from the gel and purified with the aid of the ~~Qiagen~~ QIAGEN nucleic acid purification column (Gel Extraction Kit, (Qiagen, Hilden, Germany). If appropriate, the eluate of 50 µL can be evaporated. The purified DNA is digested as follows for 2 hours at 37°C:

In the specification at page 53, line 3, please replace the paragraph which starts with "PtxA promoter" with the following amended paragraph:

PtxA promoter fragment in the Topo vector (Invitrogen) is digested with *Asc*I and *Xba*I at 37°C for 2h or 4°C overnight. The promoter fragment was purified from the gel (~~Qiagen~~ QIAGEN kit, Qiagen) after electrophoresis and cloned into upstream of GUS reporter gene in pUC using Rapid Ligation kit (Roche). The ligation solution is transformed into *E.coli* DH5α cells (Stratagene). The GUS chimeric constructs in pUC are digested with *Asc*I and *Pme*I for and cloned into a binary vector. SbHRGP3 is cloned into *Xba*I and *Bgl*II sites in a binary vector to generate the GUS chimeric construct.

In the specification at page 56, line 21, please replace the paragraph which starts with "Total RNA" with the following amended paragraph:

Total RNA is extracted from plant tissues using ~~Qiagen~~ QIAGEN RNA purification column (RNeasy® Plant Mini Kit, (Cat. No 74904, Qiagen). Quality and quantity of the RNA are determined using Molecular Probes RiboGreen Kit (Cat. No. R-11490) on the Spectra MAX Gemini. One µg of RNA is used for RT-PCR (Roche RT-PCR AMV kit, Cat. No. 1483188) in the reaction solution I under the optimized PCR program described below.

Please replace the table at page 59 of the specification with the following amended table:

Motif Name	Location (Strand)	Motif Sequence	SEQ ID NO:
AMYBOX2	537 (+)	TATCCAT	30
C8GCARGAT	571 (+/-)	CWWWWWWWWG	31
CAATBOX1	368(+); 439, 525 (-)	CAAT	32
CARGCW8GAT	571 (+/-)	CWWWWWWWWG	33
CCAATBOX1	367 (+)	CCAAT	34
DOFCOREZM	334, 357, 382, 389, 400, 429 (+); 446, 517, 591 (-)	AAAG	35
EBOXBNNAPA	407, 409 (+); 407, 409 (-)	CANNTG	36
GATABOX	337 (+), 537 (-)	GATA	37
GT1CONSENSUS	424, 544 (+); 363, 518,	GRWAAW	38

	593 (-)		
GTGANTG10	406, 452 (-)	GTGA	39
GTGANTG10	479 (-)	GTGA	39
IBOX	535 (-)	GATAAG	40
IBOXCORE	536 (-)	GATAA	41
IBOXCORENT	534 (-)	GATAAGR	42
MYBST1	537 (-)	GGATA	43
MYCATERD1	409 (+); 407 (-)	CATGTG	44
MYCATRD22	407 (+); 409 (-)	CACATG	45
MYCCONSENSUSAT	407 (+)	CANNTG	46
MYCCONSENSUSAT	409 (+); 407, 409 (-)	CANNTG	46
POLASIG1	550 (+)	AATAAA	47
POLASIG2	396 (+)	AATTAAA	48
POLASIG3	462 (+)	AATAAT	49
POLLEN1LELAT52	359 (+); 595 (-)	AGAAA	50
PYRIMIDINEBOXOSRAMY1A	590 (+)	CCTTTT	51
SEBFCONSSTPR10A	476 (+)	YTGTCWC	52
SEF4MOTIFGM7S	301 (+)	RTTTTTR	53
TAAAGSTKST1	388, 399 (+)	TAAAG	54
TATABOX5	549 (-)	TTATTT	55
TATCCAOSAMY	537 (+)	TATCCA	56
TATCCAYMOTIFOSRAMY3D	537 (+)	TATCCAY	57

Please replace the table at pages 60-61 of the specification with the following amended table:

Motif Name	Location (Strand)	Motif Sequence	SEQ ID NO:
-300ELEMENT	856 (+)	TGHAAARK	58
AMYBOX1	841 (-)	TAACARA	59
ARFAT	1166 (+)	TGTCTC	60
BOXIINTPATPB	966 (+)	ATAGAA	61
C8GCARGAT	1014 (+/-)	CWWWWWWWWG	31
CAATBOX1	801, 1014, 1228, 1234 (+); 996, 1212, 1258, 1274 (-)	CAAT	32
CARGCW8GAT	1014 (+/-)	CWWWWWWWWG	33
CCAATBOX1	1212 (-)	CCAAT	34
DOFCOREZM	852, 859, 931, 1026, 1080, 1339, 1349 (+)	AAAG	35
DOFCOREZM	825, 951, 1189 (-)	AAAG	35
GARE1OSREP1	841 (-)	TAACAGA	62
GATABOX	868, 915, 1283, 1311, 1324 (+)	GATA	37
GATABOX	1172, 1231 (-)	GATA	37
GT1CONSENSUS	1083, 1283, 1311, 1324, 1332 (+)	GRWAAW	38
GT1CONSENSUS	1104, 1131, 1149, 1238 (-)	GRWAAW	38
GTGANTG10	855, 989 (+) ; 936 (-)	GTGA	39
IBOXCORE	1283, 1311, 1324 (+)	GATAA	41
INRNTPSADB	852, 976 (-)	YTCANTYY	63
MARTBOX	1124 (+)	TTWTWTTWTT	64
MYB1LEPR	1119 (+)	GTTAGTT	65
MYBCORE	842 (+)	CNGTTR	66
MYBPLANT	1301 (+)	MACCWAMC	67
MYBPZM	1303 (+)	CCWACC	68

MYBST1	1323 (+)	GGATA	43
PALBOXPPC	1190 (+)	YTYYMMCMAMCMMC	69
POLASIG1	1049, 1128 (-)	AATAAA	47
POLASIG2	1054 (-)	AATTAAA	48
POLASIG3	1015 (+); 1146 (-)	AATAAT	49
POLLEN1LELAT52	1082 (+); 1133 (-)	AGAAA	50
PYRIMIDINEBOXOSRAMY1A	930 (-)	CCTTTT	51
QELEMENTZMZM13	933 (+)	AGGTCA	70
RAV1AAT	1100, 1355 (+)	CAACA	71
RBCSCONSENSUS	1177 (+)	AATCCAA	72
REALPHALGLHCB21	1197 (+)	AACCAA	73
ROOTMOTIFTAPOX1	540, 811, 1046, 1236(+); 802, 1229, 12135(-)	ATATT	74
RYREPEATBNNAPA	940 (+)	CATGCA	75
RYREPEATGMGY2	940 (+)	CATGCAT	76
RYREPEATLEGUMINBOX	940 (+)	CATGCAY	77
SEBFCONSSTPR10A	1165 (+); 989 (-)	YTGTCWC	52
SEF1MOTIF	1046 (+)	ATATTTAWW	78
SV40COREENHAN	1189 (-)	GTGGWWHG	79
TAAAGSTKST1	1079, 1348 (+); 951 (-)	TAAAG	54
TATABOX4	1042 (-)	TATATAA	80
TATABOX5	1050, 1124, 1129, 1147 (+); 1085 (-)	TTATTT	55
TATAPVTRNALEU	1041 (+)	TTTATATA	81
TATCCAOSAMY	1322 (-)	TATCCA	56
TGTCACACMCUCUMISIN	988 (-)	TGTCACA	82
TRANSINITDICOTS	889 (-)	AMNAUGGC	83
TRANSINITMONOCOTS	889 (-)	RMNAUGGC	84
WBOXATNPR1	1021 (+); 1098 (-)	TTGAC	85
WUSATAg	845 (+)	TTAATGG	86